

Please amend the claims as follows.

1. (Amended) A fusion protein comprising

(a) at least one binding domain comprising an antibody or binding site that specifically recognizes [specifically recognizing] an epitope of a plant pathogen; and

(b) a membrane localization sequence and/or motif that leads to membrane anchoring [at least one further domain comprising a protein or peptide sequence which is toxic to the pathogen or detrimental to its replication, transmission or life cycle].

2. (Amended) The fusion protein of claim 1 further comprising at least one domain comprising a protein or peptide sequence that is toxic to the pathogen or detrimental to its replication, transmission or life cycle [wherein said domains are linked by covalent or non-covalent bonds].

3. (Amended) The fusion protein of claim [1 or] 2 wherein the toxic activity of the protein or peptide sequence is activated by the presence of the pathogen, a component thereof or a component of a host cell.

9. (Amended) The fusion protein of claim [1] 2 wherein the toxin is an enzyme or a viral structural or non-structural protein

B2  
could be  
GAC13  
or a binding domain comprising an antibody or binding site that specifically recognizes an epitope of a plant pathogen [as defined in claim 1].

B3  
14. (Amended) A pathogenicide comprising the fusion protein of claim 1 or 2 [at lease one binding and/or further domain as defined in claim 1 and a cellular targeting sequence and/or membrane localisation sequence and/or motif that leads to membrane anchoring].

Please add the following new claims.

--38. The fusion protein of claim 1 or 2, wherein the membrane localization sequence is proteolytically sensitive.

B4  
39. The fusion protein of claim 1 or 2, wherein the membrane localization sequence is a member of the immunoglobulin super family.

40. The fusion protein of claim 1 or 2, wherein the membrane localization sequence is human T cell receptor transmembrane domains, glyco-phosphatidyl inositol (GPI) anchors, KAR1, middle-T antigen, cytochrome b5 or syn1.